Sequence Alignment

```
ABP69565
   ABP69565 standard; protein; 704 AA.
XX
AC
    ABP69565;
XX
DT
    15-JUN-2007 (revised)
    20-JAN-2003 (first entry)
DT
ХX
DE
    Human polypeptide SEQ ID NO 1612.
XX
KW
    Human; genome mapping; gene therapy; food supplement; virus; fungus;
KW
    cell-proliferative disorder; neurodegenerative disease; bacterial;
KM
    Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW
    multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW
    arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
KM
    antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW
    haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
KW
    antiarthritic; BOND PC; axotrophin;
KW
    membrane-associated RING-CH protein VII; axotrophin [Homo sapiens];
KW
    MARCH7; AXO; MARCH-VII; DKFZP586F1122; AXOT; RNF177;
KW
    membrane-associated ring finger (C3HC4) 7, isoform CRA a;
KW
    membrane-associated ring finger (C3HC4) 7, isoform CRA_a [Homo sapiens];
KW
    unknown; unknown [Homo sapiens];
KW
    membrane-associated ring finger (C3HC4) 7;
KW
    Membrane-associated ring finger (C3HC4) 7 [Homo sapiens];
KW
    unnamed protein product; unnamed protein product [Homo sapiens]; GO5515;
KM
    G06512; G08270; G016874; G046872; G04842; G06378.
XX
OS
    Homo sapiens.
XX
PN
    WO200270539-A2.
XX
PD
    12-SEP-2002.
XX
PF
    05-MAR-2002; 2002WO-US005095.
XX
PR
   05-MAR-2001; 2001US-00799451.
XX
PA
    (HYSE-) HYSEO INC.
XX
PΤ
     Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao OA, Ren F;
PΙ
    Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PΤ
    Wehrman T, Wang J, Wang D, Drmanac RT;
YY
DR
    WPI: 2002-759812/82.
DR
    N-PSDB: ABZ11782.
DR
    PC:NCBI: gi12383066.
DR
    PC:SWISSPROT; Q9H992.
XX
PT
    New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative,
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT
    or coaqulation disorders.
```

Claim 9; SEQ ID NO 1612; 1012pp + Sequence Listing; English.

The invention relates to an isolated polynucleotide (I) comprising a nucleotide sequence selected from any of 948 sequences (ABZ11119-ABZ12066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight markers, as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cellproliferative disorders (cancer), neurodegenerative diseases (Parkinson's or Alzheimer's disease), autoimmune diseases (multiple sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid disorders, platelet or coagulation disorders, wound, burns, incision, ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal, parasitic), arthritis, etc. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published pct sequences

Revised record issued on 15-JUN-2007: Enhanced with precomputed information from BOND.

SQ Sequence 704 AA;

XX PS

CC

XX

Db

Query Match 100.0%; Score 3584; DB 5; Length 704; Best Local Similarity 100.0%; Pred. No. 3.5e-269; Matches 704; Conservative 0; Mismatches 0; Indels 0; Gaps 0: 1 MESKPSRIPRRISVOPSSSLSARMMSGSRGSSLNDTYHSRDSSFRLDSEYOSTSASASAS 60 0v 1 MESKPSRIPRRISVQPSSSLSARMMSGSRGSSLNDTYHSRDSSFRLDSEYQSTSASASAS 60 Db Qу 61 PFOSAWYSESEITOGARSRSONOORDHDSKRPKLSCTNCTTSAGRNVGNGLNTLSDSSWR 120 61 PFQSAWYSESEITQGARSRSQNQQRDHDSKRPKLSCTNCTTSAGRNVGNGLNTLSDSSWR 120 Db Qv 121 HSOVPRSSSMVLGSFGTDLMRERRDLERRTDSSISNLMDYSHRSGDFTTSSYVODRVPSY 180 Db 121 HSOVPRSSSMVLGSFGTDLMRERRDLERRTDSSISNLMDYSHRSGDFTTSSYVODRVPSY 180 Qv 181 SQGARPKENSMSTLQLNTSSTNHQLPSEHQTILSSRDSRNSLRSNFSSRESESSRSNTQP 240 Db 181 SQGARPKENSMSTLQLNTSSTNHQLPSEHQTILSSRDSRNSLRSNFSSRESESSRSNTQP 240 0v 241 GFSYSSRDEAPIISNSERVVSSQRPFQESSDNEGRRTTRRLLSRIASSMSSTFFSRRSS 300 Db 241 GFSYSSSRDEAPIISNSERVVSSORPFOESSDNEGRRTTRRLLSRIASSMSSTFFSRRSS 300 Qу 301 ODSLNTRSLNSENSYVSPRILTASOSRSNVPSASEVPDNRASEASOGFRFLRRRWGLSSL 360 Db 301 ODSLNTRSLNSENSYVSPRILTASOSRSNVPSASEVPDNRASEASOGFRFLRRRWGLSSL 360 361 SHNHSSESDSENFNOESEGRNTGPWLSSSLRNRCTPLFSRRREGRDESSRIPTSDTSSR 420 0v

361 SHNHSSESDSENFNOESEGRNTGPWLSSSLRNRCTPLFSRRREGRDESSRIPTSDTSSR 420

Qу	421	SHIFRRESNEVVHLEAQNDPLGAAANRPQASAASSSATTGGSTSDSAQGGRNTGISGILP	480
Db	421	${\tt SHIFRRESNEVVHLEAQNDPLGAAANRPQASAASSSATTGGSTSDSAQGGRNTGISGILP}$	480
Qy	481	GSLFRFAVPPALGSNLTDNVMITVDIIPSGWNSADGKSDKTKSAPSRDPERLQKIKESLL	540
Db	481	${\tt GSLFRFAVPPALGSNLTDNVMITVDIIPSGWNSADGKSDKTKSAPSRDPERLQKIKESLL}$	540
Qy	541	LEDSEEEEGDLCRICQMAAASSSNLLIEPCKCTGSLQYVHQDCMKKWLQAKINSGSSLEA	600
Db	541	LEDSEEEEGDLCRICQMAAASSSNLLIEPCKCTGSLQYVHQDCMKKWLQAKINSGSSLEA	600
Qy	601	VTTCELCKEKLELNLEDFDIHELHRAHANEQAEYEFISSGLYLVVLLHLCEQSFSDMMGN	660
Db	601	VTTCELCKEKLELNLEDFDIHELHRAHANEQAEYEFISSGLYLVVLLHLCEQSFSDMMGN	660
Qy	661	TNEPSTRVRFINLARTLQAHMEDLETSEDDSEEDGDHNRTFDIA 704	
Db	661		